

TECH CENTER 1600/2900

RAW SEQUENCE LISTING
PATENT APPLICATION: US/09/768,781

DATE: 05/30/2001
TIME: 15:14:34

Input Set : A:\Seqlist.txt
Output Set: C:\CRF3\05302001\I768781.raw

ENTERED

4 <110> APPLICANT: MERKULOV, Gennady V. et al
6 <120> TITLE OF INVENTION: ISOLATED HUMAN TRANSPORTER PROTEINS,
7 NUCLEIC ACID MOLECULES ENCODING HUMAN TRANSPORTER PROTEINS,
8 AND USES THEREOF
10 <130> FILE REFERENCE: CL001057-CIP
12 <140> CURRENT APPLICATION NUMBER: 09/768,781
13 <141> CURRENT FILING DATE: 2001-01-25
15 <160> NUMBER OF SEQ ID NOS: 7
17 <170> SOFTWARE: FastSEQ for Windows Version 4.0
19 <210> SEQ ID NO: 1
20 <211> LENGTH: 1350
21 <212> TYPE: DNA
22 <213> ORGANISM: Human
24 <400> SEQUENCE: 1
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26 gaagatgtca tccgtggagc caacccccga tttacttttc catttagcat ccttttctcc 120
27 acctttttgt actgtgggga ggctgcatct gctttgtaca tggttagaat ctatcgaaag 180
28 aatagtgaag cttaccggat gacatacacc ttttctttct ttatgttttc atccattatg 240
29 gtccagttga ccctcatttt tgtccacaga gatctagcca aagataaacc gctatcatta 300
30 tttatgcata taatcctctt gggacctgtt atcagatgtt tggaggccat gattaagtac 360
31 ctacactgtt ggaagaaaga ggagcaggag gagccctatg tcagcctcac ccgaaagaag 420
32 atgctaatag atggcgagga ggtgctgata gaatgggagg tgggccactc catccggacc 480
33 ctggctatgc accgcaatgc ctacaaacgt atgtcacaga tccaagcctt cctgggctca 540
34 gtgccccagc tgacctatca gctctatgtg agcctgatct ctgcagaggt tcccctgggt 600
35 agagttgtgc taatggtatt ttccctggta tctgtcacct atggggccac cctttgcaat 660
36 atgttggtca tccagatcaa gtacgatgac tacaagattc gccttgggcc actagaagtc 720
37 ctctgcatca ccatctggcg gacattggag atcacttccc gcctcctgat tctggtgctc 780
38 ttctcagcca ctttgaaatt gaaggctgtg cccttctctag tgctcaactt cctgatcacc 840
39 ctctttgagc cctggattaa gttctggaga agtggtgccc agatgcccaa taacattgag 900
40 aaaaacttca gccgggtcgg cactctggtg gtctgtattt cagtcacat cctctatgct 960
41 ggcatacaact tctcttgctg gtcagctttg cagttgaggt tggcagacag agatctcgctc 1020
42 gacaaagggc agaactggg acatatgggc ctgcactata gtgtgaggtt ggtagagaat 1080
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44 tccttgattg ccttgcaact cattattgct tatctgattt ccattgactt catgctcctt 1200
45 ttcttccagt acttgcatcc attgcgtcca ctcttcaccc ataatgtagt agactacctc 1260
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50 <211> LENGTH: 1389
51 <212> TYPE: DNA
52 <213> ORGANISM: Human
54 <400> SEQUENCE: 2
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56 cctgaggagc caaatgtgga tccggtttca tctctggagg aagatgtcat ccgtggagcc 120
57 aacccccgat ttacttttcc atttagcatc cttttctcca cctttttgta ctgtggggag 180
58 gctgcatctg ctttgtacat ggtagaatac tatcgaaaga atagtgaac ttactggatg 240
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60 gtccacagag atctagccaa agataaacccg ctatcattat ttatgcatct aatcctcttg 360
61 ggacctgtta tcagatgttt ggaggccatg attaatgacc tcacactgtg gaagaaagag 420
62 gagcaggagg agccctatgt cagcctcacc cgaaagaaga tgctaataga tggcgaggag 480
63 gtgctgatag aatgggagggt gggccactcc atccggaccc tggctatgca ccgcaatgcc 540
64 tacaaacgta tgtcacagat ccaagccttc ctgggctcag tgccccagct gacctatcag 600
65 ctctatgtga gcctgatctc tgcagagggt cccctgggta gagttgtgct aatggtattt 660
66 tccctgggat ctgtcaccta tggggccacc ctttgcaata tgttggtat ccagatcaag 720
67 tacgatgact acaagattcg ccttgggcca ctagaagtcc tctgcatcac catctggcgg 780
68 acattggaga tcaattcccg cctcctgatt ctggtgctct tctcagccac tttgaaattg 840
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71 actctggtgg tcttgatttc agtcaccatc ctctatgctg gcatcaactt ctcttgctgg 1020
72 tcagctttgc agttgaggtt ggcagacaga gatctcgtcg acaaagggca gaactgggga 1080
73 catatgggcc tgcactatag tgtgaggttg gtagagaatg tgatcatggt cttgggtttt 1140
74 aagttctttg gagtgaaagt gttactgaat tactgtcatt ccttgattgc cttgcagctc 1200
75 attattgctt atctgatttc cattggcttc atgtcccttt tcttcagta cttgcatcca 1260
76 ttgcgctcac tcttcaccca taatgtagta gactacctcc attgtgtctg ctgtcaccag 1320
77 caccctcgga ccagggttga gaactcagag ccacccttg agactgaagc aaggcaaagt 1380
78 gttgtctga                                     1389

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80 <210> SEQ ID NO: 3

81 <211> LENGTH: 449

82 <212> TYPE: PRT

83 <213> ORGANISM: Human

85 <400> SEQUENCE: 3

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87 1 5 10 15
88 Ser Ser Leu Glu Glu Asp Val Ile Arg Gly Ala Asn Pro Arg Phe Thr
89 20 25 30
90 Phe Pro Phe Ser Ile Leu Phe Ser Thr Phe Leu Tyr Cys Gly Glu Ala
91 35 40 45
92 Ala Ser Ala Leu Tyr Met Val Arg Ile Tyr Arg Lys Asn Ser Glu Thr
93 50 55 60
94 Tyr Arg Met Thr Tyr Thr Phe Ser Phe Phe Met Phe Ser Ser Ile Met
95 65 70 75 80
96 Val Gln Leu Thr Leu Ile Phe Val His Arg Asp Leu Ala Lys Asp Lys
97 85 90 95
98 Pro Leu Ser Leu Phe Met His Leu Ile Leu Leu Gly Pro Val Ile Arg
99 100 105 110
100 Cys Leu Glu Ala Met Ile Lys Tyr Leu Thr Leu Trp Lys Lys Glu Glu
101 115 120 125
102 Gln Glu Glu Pro Tyr Val Ser Leu Thr Arg Lys Lys Met Leu Ile Asp
103 130 135 140
104 Gly Glu Glu Val Leu Ile Glu Trp Glu Val Gly His Ser Ile Arg Thr
105 145 150 155 160
106 Leu Ala Met His Arg Asn Ala Tyr Lys Arg Met Ser Gln Ile Gln Ala
107 165 170 175
108 Phe Leu Gly Ser Val Pro Gln Leu Thr Tyr Gln Leu Tyr Val Ser Leu
109 180 185 190
110 Ile Ser Ala Glu Val Pro Leu Gly Arg Val Val Leu Met Val Phe Ser

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111          195          200          205
112 Leu Val Ser Val Thr Tyr Gly Ala Thr Leu Cys Asn Met Leu Ala Ile
113          210          215          220
114 Gln Ile Lys Tyr Asp Asp Tyr Lys Ile Arg Leu Gly Pro Leu Glu Val
115 225          230          235          240
116 Leu Cys Ile Thr Ile Trp Arg Thr Leu Glu Ile Thr Ser Arg Leu Leu
117          245          250          255
118 Ile Leu Val Leu Phe Ser Ala Thr Leu Lys Leu Lys Ala Val Pro Phe
119          260          265          270
120 Leu Val Leu Asn Phe Leu Ile Ile Leu Phe Glu Pro Trp Ile Lys Phe
121          275          280          285
122 Trp Arg Ser Gly Ala Gln Met Pro Asn Asn Ile Glu Lys Asn Phe Ser
123          290          295          300
124 Arg Val Gly Thr Leu Val Val Leu Ile Ser Val Thr Ile Leu Tyr Ala
125 305          310          315          320
126 Gly Ile Asn Phe Ser Cys Trp Ser Ala Leu Gln Leu Arg Leu Ala Asp
127          325          330          335
128 Arg Asp Leu Val Asp Lys Gly Gln Asn Trp Gly His Met Gly Leu His
129          340          345          350
130 Tyr Ser Val Arg Leu Val Glu Asn Val Ile Met Val Leu Val Phe Lys
131          355          360          365
132 Phe Phe Gly Val Lys Val Leu Asn Tyr Cys His Ser Leu Ile Ala
133          370          375          380
134 Leu Gln Leu Ile Ile Ala Tyr Leu Ile Ser Ile Asp Phe Met Leu Leu
135 385          390          395          400
136 Phe Phe Gln Tyr Leu His Pro Leu Arg Ser Leu Phe Thr His Asn Val
137          405          410          415
138 Val Asp Tyr Leu His Cys Val Cys Cys His Gln His Pro Arg Thr Arg
139          420          425          430
140 Val Glu Asn Ser Glu Pro Pro Phe Glu Thr Glu Ala Arg Gln Ser Val
141          435          440          445
142 Val
146 <210> SEQ ID NO: 4
147 <211> LENGTH: 462
148 <212> TYPE: PRT
149 <213> ORGANISM: Human
151 <400> SEQUENCE: 4
152 Met Asn Thr Arg Pro Gln His Ser Glu Arg Thr Ser Thr Met Asp Arg
153 1          5          10          15
154 Val Tyr Glu Ile Pro Glu Glu Pro Asn Val Asp Pro Val Ser Ser Leu
155          20          25          30
156 Glu Glu Asp Val Ile Arg Gly Ala Asn Pro Arg Phe Thr Phe Pro Phe
157          35          40          45
158 Ser Ile Leu Phe Ser Thr Phe Leu Tyr Cys Gly Glu Ala Ala Ser Ala
159          50          55          60
160 Leu Tyr Met Val Arg Ile Tyr Arg Lys Asn Ser Glu Thr Tyr Trp Met
161 65          70          75          80
162 Thr Tyr Thr Phe Ser Phe Phe Met Phe Ser Ser Ile Met Val Gln Leu
163          85          90          95

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```

164 Thr Leu Ile Phe Val His Arg Asp Leu Ala Lys Asp Lys Pro Leu Ser
165          100          105          110
166 Leu Phe Met His Leu Ile Leu Leu Gly Pro Val Ile Arg Cys Leu Glu
167          115          120          125
168 Ala Met Ile Lys Tyr Leu Thr Leu Trp Lys Lys Glu Glu Gln Glu Glu
169          130          135          140
170 Pro Tyr Val Ser Leu Thr Arg Lys Lys Met Leu Ile Asp Gly Glu Glu
171 145          150          155          160
172 Val Leu Ile Glu Trp Glu Val Gly His Ser Ile Arg Thr Leu Ala Met
173          165          170          175
174 His Arg Asn Ala Tyr Lys Arg Met Ser Gln Ile Gln Ala Phe Leu Gly
175          180          185          190
176 Ser Val Pro Gln Leu Thr Tyr Gln Leu Tyr Val Ser Leu Ile Ser Ala
177          195          200          205
178 Glu Val Pro Leu Gly Arg Val Val Leu Met Val Phe Ser Leu Val Ser
179          210          215          220
180 Val Thr Tyr Gly Ala Thr Leu Cys Asn Met Leu Ala Ile Gln Ile Lys
181 225          230          235          240
182 Tyr Asp Asp Tyr Lys Ile Arg Leu Gly Pro Leu Glu Val Leu Cys Ile
183          245          250          255
184 Thr Ile Trp Arg Thr Leu Glu Ile Thr Ser Arg Leu Leu Ile Leu Val
185          260          265          270
186 Leu Phe Ser Ala Thr Leu Lys Leu Lys Ala Val Pro Phe Leu Val Leu
187          275          280          285
188 Asn Phe Leu Ile Ile Leu Phe Glu Pro Trp Ile Lys Phe Trp Arg Ser
189          290          295          300
190 Gly Ala Gln Met Pro Asn Asn Ile Glu Lys Asn Phe Ser Arg Val Gly
191 305          310          315          320
192 Thr Leu Val Val Leu Ile Ser Val Thr Ile Leu Tyr Ala Gly Ile Asn
193          325          330          335
194 Phe Ser Cys Trp Ser Ala Leu Gln Leu Arg Leu Ala Asp Arg Asp Leu
195          340          345          350
196 Val Asp Lys Gly Gln Asn Trp Gly His Met Gly Leu His Tyr Ser Val
197          355          360          365
198 Arg Leu Val Glu Asn Val Ile Met Val Leu Val Phe Lys Phe Phe Gly
199          370          375          380
200 Val Lys Val Leu Leu Asn Tyr Cys His Ser Leu Ile Ala Leu Gln Leu
201 385          390          395          400
202 Ile Ile Ala Tyr Leu Ile Ser Ile Gly Phe Met Leu Leu Phe Phe Gln
203          405          410          415
204 Tyr Leu His Pro Leu Arg Ser Leu Phe Thr His Asn Val Val Asp Tyr
205          420          425          430
206 Leu His Cys Val Cys Cys His Gln His Pro Arg Thr Arg Val Glu Asn
207          435          440          445
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209          450          455          460
212 <210> SEQ ID NO: 5
213 <211> LENGTH: 17993
214 <212> TYPE: DNA

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215 <213> ORGANISM: Human

217 <220> FEATURE:

218 <221> NAME/KEY: misc_feature

219 <222> LOCATION: (1)...(17993)

220 <223> OTHER INFORMATION: n = A,T,C or G

222 <400> SEQUENCE: 5

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225 cctgagtagc tgggattaca gtcacgcacc accacgacca gctgattttt gtatttttag 180
226 tagagatggg gtttcaccac gttggccagg ctggtttcga actcctgacc tcaagtgtac 240
227 tgcctgcctc agcctcccaa agtgctggga ttacaggcgt gaaccactgt gcctggcctt 300
228 catctatatt attaccagga ggcagatgtg ttctcttttt ctctgagggt tagaattatg 360
229 caaatgaaga tatgaaaaca aaagctcagt gaggtgggga ggattacact taagaataca 420
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VERIFICATION SUMMARY

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Input Set : A:\Seqlist.txt

Output Set: C:\CRF3\05302001\I768781.raw

L:509 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5

L:510 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5